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REMARKS

Claims 1-87 are pending and under examination. Claim 21 has been amended. The amendment merely corrects the dependency of claim 21 and is supported throughout the specification and the claims as filed. The specification has been amended to correct typographical errors and to insert SEQ ID NOS corresponding the Sequence Listing submitted herewith. Accordingly, these amendments do not raise an issue of new matter and entry thereof is respectfully requested.

Applicant brings to the Examiner's attention co-pending application serial no. 09/747,174.

Objections to the Specification

The objections to the specification are respectfully traversed. Regarding the objection for lack of compliance with the sequence rules, the specification has been amended to assign SEQ ID NOS to the sequences disclosed in the application. The corresponding Sequence Listing is being submitted herewith.

With regard to the objection of the term "[12]" on page 78, line 17, the specification has been amended to delete this term. Accordingly, it is respectfully requested that this objection be withdrawn.

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Regarding the objection to the alleged use of embedded hyperlink and/or other form of browser-executable code, the Office Action indicates that the embedded hyperlink should be deleted. Referring to MPEP § 608.1, it is indicated that hyperlinks and other forms of browser-executable code are not permitted in a patent application so that the term can be interpreted as a valid HTML code and become a live web link in the electronic presentation of the patent application or patent on the USPTO web page. MPEP § 608.01 exemplifies a hyperlink or browser-executable code as a URL (universal resource locator) placed between the symbols "<>" or after "http://." However, the website recited on page 22, line 24, for the National Center for Biotechnology Information is not embedded in a hyperlink or other form of browser-executable code and therefore cannot function as a live web link on an electronic copy of the published application or patent on the USPTO website. Accordingly, it is respectfully requested that this objection be withdrawn.

Objection to the Claims

The objection to claim 21 is respectfully traversed. Claim 21 has been amended to depend from claim 20, as suggested by the Examiner. Accordingly, it is respectfully requested that this objection be withdrawn.

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Rejections Under 35 U.S.C. § 102

The rejection of claims 1, 4, 6, 11 and 12 under 35 U.S.C. § 102 as allegedly anticipated by Corpet et al., Nucl. Acids Res. 28:267-269 (2000), Henikoff et al., Nucl. Acids Res. 28:228-230 (2000), or Murzin et al., J. Mol. Biol. 247:536-540 (1995), is respectfully traversed. Applicants submit that these claims are novel over any of Corpet et al., Henikoff et al., or Murzin et al.

Applicants submit that neither of Corpet et al., Henikoff et al., or Murzin et al. teaches the claimed methods for separating two or more subsets of polypeptides within a set of polypeptides, as recited in claim 1. At best, Corpet et al. describes the ProDom database of protein domain families but not the claimed method using a sequence comparison signature. With regard to Henikoff et al., this reference describes the Blocks database, which uses ungapped multiple alignments corresponding to the most conserved regions of proteins but not the claimed method. Regarding Murzin et al., this reference describes the Structural Classification of Proteins (SCOP) database, which is based on the known structures of proteins. However, none of Corpet et al., Henikoff et al., or Murzin et al. teaches the claimed methods for separating two or more subsets of polypeptides within a set of polypeptides using a sequence comparison signature. Absent such a teaching, none of Corpet et al., Henikoff et al., or Murzin

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et al. can anticipate the claims. Accordingly, Applicants respectfully request that this rejection be withdrawn.

The rejection of claims 1, 4, 6, 11 and 12 under 35 U.S.C. § 102(a) as allegedly anticipated by Apweiler et al., Nucl. Acids Res. 29:44-48 (2001), or Bejerano et al., Bioinformatics 17:927-934 (2001), is respectfully traversed. Applicants submit that these claims are novel over Apweiler et al. or Bejerano et al.

Applicants submit that neither of Apweiler et al. or Bejerano et al. teaches the claimed methods for separating two or more subsets of polypeptides within a set of polypeptides, as recited in claim 1. At best, Apweiler et al. describes online tools such as InterPro and CluSTr for analysis of whole genomes. With regard to Bejerano et al., this reference describes a method for automatically detecting protein domains and clustering protein sequences by these domains. However, neither of Apweiler et al. nor Bejerano et al. teaches the claimed methods for separating two or more subsets of polypeptides within a set of polypeptides using a sequence comparison signature. Absent such a teaching, neither Apweiler et al. nor Bejerano et al. can anticipate the claims. Accordingly, Applicants respectfully request that this rejection be withdrawn.

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Rejections Under 35 U.S.C. § 103

The rejection of claims 2, 3, 5, 7-10 and 13-24 under 35 U.S.C. § 103 as allegedly obvious over Corpet et al., *supra*, Henikoff et al., *supra*, Murzin et al., *supra*, Apweiler et al., *supra*, Bejerano et al., *supra*, in view of alleged admitted prior art is respectfully traversed. Applicants submit that these claims are unobvious over the cited references, alone or in combination with known methods.

As discussed above, none of Corpet et al., Henikoff et al., Murzin et al., Apweiler et al., or Bejerano et al. teaches or suggests the claimed methods for separating two or more subsets of polypeptides within a set of polypeptides using a sequence comparison signature, as in claim 1, nor do any of these references teach or suggest the claimed methods for identifying a member of a polypeptide family using a sequence comparison signature, as in claim 13. Moreover, none of these references, alone or in combination with known methods, teaches or suggests the claimed methods. Absent such a teaching or suggestion, none of Corpet et al., Henikoff et al., Murzin et al., Apweiler et al., or Bejerano et al., alone or in combination with known methods, can render the claimed methods obvious. Accordingly, Applicants respectfully request that this rejection be withdrawn.

The rejection of claims 25-87 under 35 U.S.C. § 103 as allegedly obvious over Corpet et al., *supra*, Henikoff et al., *supra*, Murzin et al., *supra*, Apweiler et al., *supra*, Bejerano et al., *supra*, in view of alleged admitted prior art and further in view of Böhm, J. Computer-Aided Molec. Design 6:61-78 (1992), or Carugo et al., Proteins: Struct. Function Genet. 28:10-28 (1997), is respectfully traversed. Applicants submit that these claims are unobvious over the cited references, alone or in combination with known methods.

As discussed above, none of Corpet et al., Henikoff et al., Murzin et al., Apweiler et al., or Bejerano et al. teaches or suggests the claimed methods for identifying a polypeptide pharmacofamily, for constructing a conformer model, or for predicting a bound conformation of a ligand bound to a polypeptide using a sequence comparison signature, as in independent claims 25, 37, 49, 61 and 76. Moreover, neither of the secondary references by Böhm or Carugo and Argos, alone or in combination with known methods, teaches or suggests the claimed methods. At best, Böhm describes the program LUDI and its use for designing enzyme inhibitors. Carugo and Argos describes the stereochemistry of cofactor binding to NADP-dependent enzymes. Therefore, none of Corpet et al., Henikoff et al., Murzin et al., Apweiler et al., or Bejerano et al., alone or in combination with Böhm or Carugo and Argos and/or known methods, can render the claimed methods

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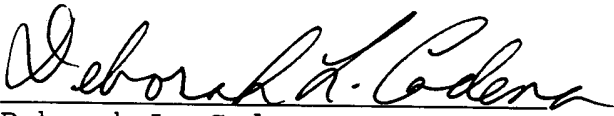
obvious. Accordingly, Applicants respectfully request that this rejection be withdrawn.

CONCLUSION

In light of the amendments and remarks herein, Applicants submit that the claims are now in condition for allowance and respectfully request a notice to this effect. The Examiner is invited to call the undersigned agent if there are any questions.

Respectfully submitted,

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Date


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